

Resource Summary Report

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Transcriptomics Explorer

RRID:SCR_017567

Type: Tool

Proper Citation

Transcriptomics Explorer (RRID:SCR_017567)

Resource Information

URL: <https://portal.brain-map.org/atlas-es-and-data/rnaseq>

Proper Citation: Transcriptomics Explorer (RRID:SCR_017567)

Description: Software tool to visualize and analyze transcriptomics data and transcriptomic cell types for mouse and human, all directly in web browser. To explore gene expression heatmap across cell types in datasets, search for genes of interest, explore tSNE visualization, colored by cell types or expression of genes of interest, visualize dataset's sampling strategy to see how cells and nuclei were sampled across brain areas, cortical layer, and other dimensions, find cell type of interest in one visualization and see its characteristics in different visualization. Used for Allen Brain Map Cell Types Database to Browse Data: Human - Multiple Cortical Areas, and Mouse - Cortex and Hippocampus.

Resource Type: software application, data processing software, data analysis software, service resource, software resource, data visualization software

Keywords: Visualize, analyze, transcriptomic, data, cell, type, mouse, human, Allen, database, multiple, cortical, area, cortex, hippocampus

Availability: Free, Freely available

Resource Name: Transcriptomics Explorer

Resource ID: SCR_017567

Alternate URLs: <https://celltypes.brain-map.org/rnaseq/human/cortex>,
<https://celltypes.brain-map.org/rnaseq/mouse/cortex-and-hippocampus>,

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260804T043704+0000

Ratings and Alerts

No rating or validation information has been found for Transcriptomics Explorer.

No alerts have been found for Transcriptomics Explorer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Kim HG, et al. (2025) The WAVE complex in developmental and adulthood brain disorders. *Experimental & molecular medicine*, 57(1), 13.

Mills WA, et al. (2025) Microglial cyclooxygenase-1 modulates cerebral capillary basal tone in vivo in mice. *Nature communications*, 16(1), 5704.

Sung E, et al. (2025) Augmenting the human interactome for disease prediction through gene networks inferred from human cell atlas. *Animal cells and systems*, 29(1), 11.

Gimenez GA, et al. (2025) A Study on Potential Sources of Perineuronal Net-Associated Sema3A in Cerebellar Nuclei Reveals Toxicity of Non-Invasive AAV-Mediated Cre Expression in the Central Nervous System. *International journal of molecular sciences*, 26(2).

García-Ruiz S, et al. (2025) Splicing accuracy varies across human introns, tissues, age and disease. *Nature communications*, 16(1), 1068.

Yang J, et al. (2025) Spotiphy enables single-cell spatial whole transcriptomics across an entire section. *Nature methods*, 22(4), 724.

Pizzamiglio L, et al. (2025) Excitatory glycine receptors control ventral hippocampus synaptic plasticity and anxiety-related behaviors. *Proceedings of the National Academy of Sciences of the United States of America*, 122(37), e2501118122.

Machold R, et al. (2024) Genetic approaches to elucidating cortical and hippocampal GABAergic interneuron diversity. *Frontiers in cellular neuroscience*, 18, 1414955.

Yokoyama K, et al. (2024) Visualization of myelin-forming oligodendrocytes in the adult mouse brain. *Journal of neurochemistry*.

Bai Z, et al. (2024) Spatially Exploring RNA Biology in Archival Formalin-Fixed Paraffin-Embedded Tissues. *bioRxiv : the preprint server for biology*.

Zhao H, et al. (2024) Identifying novel proteins for suicide attempt by integrating proteomes from brain and blood with genome-wide association data. *Neuropsychopharmacology : official publication of the American College of*

Neuropsychopharmacology, 49(8), 1255.

Montani C, et al. (2024) Sex-biasing influence of autism-associated Ube3a gene overdosage at connectomic, behavioral, and transcriptomic levels. Science advances, 10(28), eadg1421.

Tian J, et al. (2024) Hippocampal transcriptome-wide association study and pathway analysis of mitochondrial solute carriers in Alzheimer's disease. Translational psychiatry, 14(1), 250.

Pichet Binette A, et al. (2024) Proteomic changes in Alzheimer's disease associated with progressive A β plaque and tau tangle pathologies. Nature neuroscience, 27(10), 1880.

Dear R, et al. (2024) Cortical gene expression architecture links healthy neurodevelopment to the imaging, transcriptomics and genetics of autism and schizophrenia. Nature neuroscience, 27(6), 1075.

K C R, et al. (2024) Zmiz1 is a novel regulator of brain development associated with autism and intellectual disability. Frontiers in psychiatry, 15, 1375492.

Bahl E, et al. (2024) Using deep learning to quantify neuronal activation from single-cell and spatial transcriptomic data. Nature communications, 15(1), 779.

Lukacs IP, et al. (2023) Differential effects of group III metabotropic glutamate receptors on spontaneous inhibitory synaptic currents in spine-innervating double bouquet and parvalbumin-expressing dendrite-targeting GABAergic interneurons in human neocortex. Cerebral cortex (New York, N.Y. : 1991), 33(5), 2101.

Johansen N, et al. (2023) Projecting RNA measurements onto single cell atlases to extract cell type-specific expression profiles using scProjection. Nature communications, 14(1), 5192.

García-Ruiz S, et al. (2023) Splicing accuracy varies across human introns, tissues and age. bioRxiv : the preprint server for biology.